



ENTERED

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/839,073

DATE: 03/21/2003
TIME: 13:05:05

Input Set : A:\13492.seq.txt
Output Set: N:\CRF4\03212003\I839073.raw

3 <110> APPLICANT: Sacktor, Todd C.
 5 <120> TITLE OF INVENTION: A MEMORY ENHANCING PROTEIN
 7 <130> FILE REFERENCE: The Research Foundation Albany
 9 <140> CURRENT APPLICATION NUMBER: 09/839,073
C--> 10 <141> CURRENT FILING DATE: 2003-03-17
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2058
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (444)..(1670)
 25 <220> FEATURE:
 26 <221> NAME/KEY: unsure
 27 <222> LOCATION: (522)
 28 <223> OTHER INFORMATION: r at position 522 is g or a
 30 <400> SEQUENCE: 1
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 33 ttccgttaaa tatctgtcc tcgcgtcgaa gcctccctgc ctattgtcgg ggccggagcg 120
 35 aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cggccgcgc 180
 37 gcacagagca taaaagaatct ggcgttgggaa ggcaggagaa gaaagccgaa tctatctacc 240
 39 gccggggagc cagaagatgg aggaagctgt accgtgcctaa cggccacccctc ttccaagcca 300
 41 agcgctttaa caggagagcg tactgcggtc agtgcagcga gaggatatgg ggcctcgcga 360
 43 ggcaaggcta caggtgcata aactgcaaac tgctggtcca taaggcgtgc cacggcctcg 420
 45 tcccgtgac ctgcaggaag cat atg gat tct gtc atg cct tcc caa gag cct 473
 46 Met Asp Ser Val Met Pro Ser Gln Glu Pro 10
 47 1 5 10
 49 cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca 521
 50 Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr
 51 15 20 25
 53 rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa 569
W--> 54 Xaa Gly Ile Ala Tyr Ile Ser Ser Arg Lys His Asp Ser Ile Lys
 55 30 35 40
 57 gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc 617
 58 Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile
 59 45 50 55
 61 aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc 665
 62 Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val
 63 60 65 70
 66 atc ggg cgc ggg agc tac gcc aag gtt ctc ctg gtg cggttg aag aag 713
 67 Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg Leu Lys Lys

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68	75	80	85	90	
70	aat gac caa att tac gcc atg aaa gtg gtg aag aaa gag ctg gtg cat				761
71	Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val His				
72	95	100	105		
74	gat gac gag gat att gac tgg gta cag aca gag aag cac gtg ttt gag				809
75	Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe Glu				
76	110	115	120		
78	cag gca tcc agc aac ccc ttc ctg gtc gga tta cac tcc tgc ttc cag				857
79	Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe Gln				
80	125	130	135		
82	acg aca agt cgg ttg ttc ctg gtc att gag tac gtc aac ggc ggg gac				905
83	Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly Asp				
84	140	145	150		
86	ctg atg ttc cac atg cag agg cag agg aag ctc cct gag gag cac gcc				953
87	Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His Ala				
88	155	160	165	170	
90	agg ttc tac gcg gcc gag atc tgc atc gcc ctc aac ttc ctg cac gag				1001
91	Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His Glu				
92	175	180	185		
94	agg ggg atc atc tac agg gac ctg aag ctg gac aac gtc ctc ctg gat				1049
95	Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp				
96	190	195	200		
98	gcg gac ggg cac atc aag ctc aca gac tac ggc atg tgc aag gaa ggc				1097
99	Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly				
100	205	210	215		
102	ctg ggc cct ggt gac aca acg agc act ttc tgc gga acc ccg aat tac				1145
103	Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr				
104	220	225	230		
106	atc gcc ccc gaa atc ctg cgg gga gag gag tac gac ggc atc ttc acc				1193
107	Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp				
108	235	240	245	250	
110	tgg tgg gcg ctg gga gtc ctc atg ttt gag atg atg gcc ggg cgc tcc				1241
111	Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg Ser				
112	255	260	265		
114	ccg ttc gac atc atc acc gac aac ccg gac atg aac aca gag gac tac				1289
115	Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr				
116	270	275	280		
118	ctt ttc caa gtg atc ctg gag aag ccc atc cgg atc ccc cgg ttc ctg				1337
119	Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu				
120	285	290	295		
122	tcc gtc aaa gcc tcc cat gtt tta aaa gga ttt tta aat aag gac ccc				1385
123	Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp Pro				
124	300	305	310		
126	aaa gag agg ctc ggc tgc cgg cca cag act gga ttt tct gac atc aag				1433
127	Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys				
128	315	320	325	330	
131	tcc cac gcg ttc ttc cgc agc ata gac tgg gac ttg ctg gag aag aag				1481
132	Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys				
133	335	340	345		

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135 cag	gct	ctc	cct	cca	ttc	cag	cca	cag	atc	aca	gac	gac	tac	ggt	ctg	1529
136 Gln	Ala	Leu	Pro	Pro	Phe	Gln	Pro	Gln	Ile	Thr	Asp	Asp	Tyr	Gly	Leu	
137	350					355				360						
139 gac	aac	ttt	gac	aca	cag	ttc	acc	agc	gag	ccc	gtg	cag	ctg	acc	cca	1577
140 Asp	Asn	Phe	Asp	Thr	Gln	Phe	Thr	Ser	Glu	Pro	Val	Gln	Leu	Thr	Pro	
141	365					370			375							
143 gac	gat	gag	gat	gcc	ata	aag	agg	atc	gac	cag	tca	gag	ttc	gaa	ggc	1625
144 Asp	Asp	Glu	Asp	Ala	Ile	Lys	Arg	Ile	Asp	Gln	Ser	Glu	Phe	Glu	Gly	
145	380					385			390							
147 ttt	gag	tat	atc	aac	cca	tta	ttg	ctg	tcc	acc	gag	gag	tcg	gtg		1670
148 Phe	Glu	Tyr	Ile	Asn	Pro	Leu	Leu	Ser	Thr	Glu	Glu	Ser	Va			
149 395					400				405							
151 tgaggccgcg	tgcgctctg	tcgtggacac	gcgtgattga	cccttaact	gtatcctaa											1730
153 ccaccgcata	tgcatgccag	gctgggcacg	gctccgaggg	cggccaggg	cagacgcttg											1790
155 cgccgagacc	gcagagggaa	gcgtcagcgg	gcgcgtctgg	gagcagaaca	gtccctcaca											1850
157 cctggcccg	caggcagctt	cgtgtctggag	gaacttgcgt	ctgtgcctgc	gtgcggcgg											1910
159 atccgcgggg	accctgccga	gggggctgtc	atgcggttc	caaggtgcac	atttccacg											1970
161 gaaacagaac	tcgatgcact	gacctgctcc	gccaggaaag	tgagcgtgta	gcgtcctgag											2030
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167 <211>	LENGTH:	409														
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172 <221>	NAME/KEY:	unsure														
173 <222>	LOCATION:	(27)														
174 <223>	OTHER INFORMATION:	Xaa at position 27 is Asp or Asn														
177 <400>	SEQUENCE:	2														
178 Met	Asp	Ser	Val	Met	Pro	Ser	Gln	Glu	Pro	Pro	Val	Asp	Asp	Lys	Asn	
179 1				5					10					15		
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182	20						25				30					
184 Ser	Ser	Ser	Arg	Lys	His	Asp	Ser	Ile	Lys	Asp	Asp	Ser	Glu	Asp	Leu	
185	35						40				45					
187 Lys	Pro	Val	Ile	Asp	Gly	Met	Asp	Gly	Ile	Lys	Ile	Ser	Gln	Gly	Leu	
188	50						55			60						
190 Gly	Leu	Gln	Asp	Phe	Asp	Leu	Ile	Arg	Val	Ile	Gly	Arg	Gly	Ser	Tyr	
191 65				70				75				80				
193 Ala	Lys	Val	Leu	Leu	Val	Arg	Leu	Lys	Lys	Asn	Asp	Gln	Ile	Tyr	Ala	
194	85						90				95					
196 Met	Lys	Val	Val	Lys	Lys	Glu	Leu	Val	His	Asp	Asp	Glu	Asp	Ile	Asp	
197	100						105				110					
199 Trp	Val	Gln	Thr	Glu	Lys	His	Val	Phe	Glu	Gln	Ala	Ser	Ser	Asn	Pro	
200	115						120				125					
202 Phe	Leu	Val	Gly	Leu	His	Ser	Cys	Phe	Gln	Thr	Thr	Ser	Arg	Leu	Phe	
203	130						135			140						
205 Leu	Val	Ile	Glu	Tyr	Val	Asn	Gly	Gly	Asp	Leu	Met	Phe	His	Met	Gln	
206 145				150				155				160				
208 Arg	Gln	Arg	Lys	Leu	Pro	Glu	Glu	His	Ala	Arg	Phe	Tyr	Ala	Ala	Glu	

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209          165          170          175
211 Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg
212          180          185          190
214 Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys
215          195          200          205
217 Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr
218          210          215          220
220 Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu
221 225          230          235          240
223 Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val
224          245          250          255
226 Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr
227          260          265          270
229 Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu
230          275          280          285
232 Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His
233          290          295          300
235 Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys
236 305          310          315          320
238 Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg
239          325          330          335
241 Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe
242          340          345          350
244 Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln
245          355          360          365
247 Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile
248          370          375          380
250 Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro
251 385          390          395          400
253 Leu Leu Leu Ser Thr Glu Glu Ser Val
254          405
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 2058
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 3
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267 ttccggctgcg tcgttagtcga gcagttgcc ttccttctac ggagggacgt gcggggccggc 180
268 cgtgtctcgat atttctttaga cgcgactctt ccgtcctctt ctttcggctt agatagatgg 240
269 cggcccccctcg gtcttctacc tccttcgaca tggcacgggtt gccggtgag aaggttcggt 300
270 tcgcgaaattt gtcctctcgc atgacgccaag tcacgtcgct tcctatacc ccggagcgct 360
271 ccgttccgat gtccacgtag ttgacgtttt acgaccaggat attcgcgacg gtgccggagc 420
272 aggggcactg gacgtccttc gtatacctaa gacagtacgg aagggttctc ggaggtcatc 480
273 tgctgttctt gtccttcgg ctgaaaggaa ggcttcctcg tctacctaa cgaatgtaaa 540
274 ggagtagggc cttcgtagtg tcgtaatttc tgctgagcct cctggaattc ggtcaatagc 600
275 taccctacctt accttagttt tagagagttcc ccgaacccga cgtcctgaaa ctggattagt 660
276 ctcagtagcc cgcgcctcg atgcggttcc aagaggacca cgccaacttc ttcttactgg 720
277 tttaaatgcg gtactttcac cacttcttc tcgaccacgt actactgctc ctataactga 780

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278 cccatgtctg tctttcgtg cacaaactcg tccgttagtc gttgggaag gaccaggcta 840
279 atgtgaggac gaaggctgc tgttcagcca acaaggacca gtaactcatg cagttgccgc 900
280 ccctggacta caaggtgtac gtctccgtct ccttcgaggg actcctcgatg cggtccaaga 960
281 tgcgccggct ctagacgtag cgggagttga aggacgtgct ctccccctag tagatgtccc 1020
282 tggacttcga cctgttgca gaggacctac gcctgcccgt gtagttcgag tgctctgatgc 1080
283 cgtacacgtt ccttccggac cccggaccac tgtgttgctc gtgaaaagacg ccttggggct 1140
284 taatgttagcg ggggctttag gacgcccccc tcctcatgcc caagtgcac ctgaccaccc 1200
285 gcgaccctca ggagtacaaa ctctactacc ggcccgcgag gggcaagctg tagtagtggc 1260
286 tggggccct gtacttgtgt ctccctgatgg aaaaggttca ctaggacctc ttccggtagg 1320
287 cctagggggc caaggacagg cagtttcgga gggtacaaaa ttccctaaa aatttattcc 1380
288 tggggtttct ctccgagccg acggccggtg tctgaccta aagactgtag ttcaagggtgc 1440
289 gcaagaaggc gtcgtatctg accctgaacg acctcttctt cgtccgcgag ggaggtaagg 1500
290 tcgggtgtcta gtgtctgctg atgccagacc tggtgaaact gtgtgtcaag tggtcgctcg 1560
291 ggcacgtcga ctggggctcg ctactcctac ggtatttctc ctagctggtc agtctcaagc 1620
292 ttccgaaact catatagttg ggtataaaacg acaggtggct cctcagccac actccggcgc 1680
293 acgcagagac agcacctgtg cgcactaact gggaaattga cataggaatt ggtggcgtat 1740
294 acgtacggc cgaccctgtc cgaggctccc gccgggtccct gtctgcgaac gcggtctgg 1800
296 cgtccctt cgcagtcgccc cgcgacgacc ctgcgtctgt cagggagtgt ggaccgggccc 1860
297 gtccgtcgaa gcacgacctc cttgaacgac gacacggacg cagcgcgcgc taggcgcucc 1920
298 tgggacggct ccccccacag tacgccaaag gttccacgtg taaaaggtgc cttgtcttg 1980
299 agctacgtga ctggacgagg cggtccttcc actcgcacat cgcaggactc cttatttac 2040
300 aaggctactt tttttttt 2058
303 <210> SEQ ID NO: 4
304 <211> LENGTH: 13
305 <212> TYPE: PRT
306 <213> ORGANISM: Unknown Organism
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Unknown Organism: mzip peptide
311 <400> SEQUENCE: 4
312 Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu
313 1 5 10

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/839,073

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 27
Seq#:2; Xaa Pos. 27

VERIFICATION SUMMARY

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Input Set : A:\13492.seq.txt

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:569

L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16